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Results of SIM with:

Sequence 1: seq (448 residues)

Sequence 2: seq (448 residues)

using the parameters:

Comparison matrix: BLOSUM62

Number of alignments computed: 20

Gap open penalty: 12

Gap extension penalty: 4



Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH.

76.6% identity in 445 residues overlap; Score: 1857.0; Gap frequency: 0.0%

seq 1 MNMPETGPAGIASQLKLDHWMPTANRNFORDPRLIVAAEGNYLVDDHGRKIFDALSGL
seq 1 MNQPLNVAPPVSSLELNRAHWMPPSANRNFQKDPRIIVAAEGSWLTDKGRKVDLSLGL

```
seq      61  WTCGAGHTRKEIADAVTRQLSTLDYSPAQFGHPLSFQLAEKIAELVPGNLNHVFTNSG
seq      61  WTCGAGHSRKEIQEAVARQLGTLTDYSPGEQYGHPLSFQLAEKIAGLLPGELNHVFTTSG
          ***** **
```

```
seq      121 SECADTALKMVRAYWRLKGQATKTKIIGRARGYHGVNIAGTSLGGVNGNRKMFQQLLDVD
seq      121 SECADTSIKMARAYWRLKGQPKTKLIGRARGYHGVNVAGTSLGGIGGNRKMFQQLMDVD
          * * * * *
          * * * * *
```

```
seq      181 HLPHTVLPVNAFSKGLPEEGGIALADEMLKLIELHDASNIAAVIVEPLAGSAGVLPFPKG
seq      181 HLPHTLQPGMAFTRGMAQTGGVELANELKLIELHDASNIAAVIVEPMMSGAGVLPFPVG
          * * * * *
```

```
seq      241 YLKRLREICTQHNILLIFDEVITGFGRMGAMTGSEAFGVTPDLMCIAKQVNTGAIPMGAV
seq      241 YLQRLREICDQHNILLIFDEVITAFGRGTYSGAEYFGVTPDLMNVAKQVNTGAVPMGAV
          * * * * *
```

seq 301 IASSEIYQTFMNQPTPEYAVEFPHGYTSAHPVACAAGLAALDLOKENLYQSAELAPH
seq 301 IASSEIYDTFMNQALPEHAVEFPHGYTSAHPVACAAGLAALDILARDNLYQSAELAPH

```

*****
seq      361 FEKLLHGVKGTKNIVDIRNYGLAGAIQIAARDGDAIVRPYEAMKLWKAGFYVRFGGDTL
seq      361 FEKGLHGLQGAKNVIDIRNCGLAGAIQIAPRDGDPTVRPFEAGMKLWQQGFYVRFGGDTL
          * * * * *
seq      421 QFGPTENTKQELDRLEDAVGETLN
seq      421 QFGPTENARPEELDRLEDAVGEALN
          * * * * *

```

32.0% identity in 25 residues overlap; Score: 29.0; Gap frequency: 0.0%

```

seq      315 TPEYAVEEPHGYTYSAPVACAAGL
seq      82  TLDYSPGFQYGHPLSFQLAEKIAGL
          * * * * *

```

23.1% identity in 26 residues overlap; Score: 27.0; Gap frequency: 0.0%

```

seq      211 LIELHDASNTAAVIVEPLAGSAGVLP
seq      374 VIDIRNCGLAGAIQIAPRDGDPTVRP
          * * * * *

```

33.3% identity in 15 residues overlap; Score: 26.0; Gap frequency: 0.0%

```

seq      120 GSECADTALKMVRAY
seq      201 GVELANELLKIELH
          * * * *

```

25.0% identity in 28 residues overlap; Score: 26.0; Gap frequency: 0.0%

```

seq      82  TLDYSPATQFGHPLSFQLAEKIAELVPG
seq      419 TLQFGPTFNARPEELDRLEDAVGEALNG
          * * * *

```

36.4% identity in 11 residues overlap; Score: 26.0; Gap frequency: 0.0%

```

seq      400 YEAMKLWKAG
seq      54  YDSLGLWTCG
          * *

```

38.5% identity in 13 residues overlap; Score: 26.0; Gap frequency: 0.0%

```

seq      3  MPETGPAGIASQL
seq      196 MAQTGGVELANEL
          * *

```

27.3% identity in 22 residues overlap; Score: 25.0; Gap frequency: 0.0%

```

seq      253 WILLIFDEVITCFGRMCAMTGS
seq      282 DLMNVAKQVTNGAVPMGAVIAS

```

30.4% identity in 23 residues overlap; Score: 25.0; Gap frequency: 0.0%

```
seq      242 LKRLREICTQHNILLIFDEVITG
seq      208 LLKLIELHDASNIAAVIVEPMSG
      * * * * *
```

50.0% identity in 10 residues overlap; Score: 25.0; Gap frequency: 0.0%

```
seq      99 LAEKIAELVP
seq      350 LVQQSAGELAP
      * * * * *
```

30.4% identity in 23 residues overlap; Score: 25.0; Gap frequency: 0.0%

```
seq      214 LHDASNIAAVIVEPLAGSAGVLP
seq      368 LOGARNVIDIRNCGLAGAIQIAP
      * * * * *
```

50.0% identity in 8 residues overlap; Score: 24.0; Gap frequency: 0.0%

```
seq      4 PETGPAGI
seq      227 PMSGGAGV
      * * * *
```

62.5% identity in 8 residues overlap; Score: 24.0; Gap frequency: 0.0%

```
seq      385 AIQIAARD
seq      341 ALDILARD
      * * * *
```

23.3% identity in 30 residues overlap; Score: 24.0; Gap frequency: 0.0%

```
seq      63 CGAGHTRKEIADAVTRQLSTLDYSAPFQEG
seq      335 CAAGLAALDILARDNLVQQSAGELAPHFEKG
      * * * * *
```

35.3% identity in 17 residues overlap; Score: 24.0; Gap frequency: 0.0%

```
seq      210 KLIELHDASNIAAVIVE
seq      244 RLREICDOHNILLIFDE
      * * * * *
```

50.0% identity in 8 residues overlap; Score: 23.0; Gap frequency: 0.0%

```
seq      325 GYTYSANP
seq      423 GPTFNARP
      * * * *
```

100.0% identity in 4 residues overlap; Score: 23.0; Gap frequency: 0.0%

seq 311 MNQP
seq 1 MNQP

45.5% identity in 11 residues overlap; Score: 23.0; Gap frequency: 0.0%

seq 218 SNIAAVIVEPL
seq 229 SGSAGLVPPV
* * * *

50.0% identity in 8 residues overlap; Score: 23.0; Gap frequency: 0.0%

seq 419 TLQFGPTF
seq 82 TLDYSPQF
* * * *

60.0% identity in 5 residues overlap; Score: 23.0; Gap frequency: 0.0%

seq 131 VRAYW
seq 17 LRAHW
* * *

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Sequence Alignment and Identity Table **GenBank: AAG06957 and GenBank: AAA25891**

```

AAA25891      (1) 1 MSVPVRHLIAGAFVEGLGAQRIPVSNPLDNSTLAEIACASAEQVEQAVAS 50
AAG06957      (1) -----
Consensus     (1)

AAA25891      (51) 51 ARETFASWKETPVSERARVMLRYQALLKEHHDELAKIVSSELGKTFEDAK 100
AAG06957      (1) -----
Consensus     (51)

AAA25891     (101) 101 GDVWRGIEVVEHACNVPSLLMGETVENVARNIDTYSITQPLGVCVGITPF 150
AAG06957      (1) -----
Consensus     (101)

AAA25891     (151) 151 NFPAMIPLWMFPLAIACGNAFILKPSEQVPLTSVRLAELFLEAGAPKIVL 200
AAG06957      (1) -----MTDIIFL
Consensus     (151) A L

AAA25891     (201) 201 QVHGGKEQVDLLKHPOVKAVSF GSVAVGQYVYHTT HNKRQSFAQ 250
AAG06957      (8) GGNMGGPMAALLKAGHRVNVFD QPKAVLGLVEQG QADSAQCCEQ
Consensus     (201) L G NLLK V L AV V A A LQ G

AAA25891     (251) 251 AKNHVDPDKAQVSNLVGSAQAQC AISVVVGAAREWPE 300
AAG06957      (58) AEVVSPAPQHVESYLGDDL RVGP LIDCT APETARKAE
Consensus     (251) A I ILP A I A LA A K L I A I I E

AAA25891     (301) 301 IRDALKVRPGP-----WDDGASYGPVINPQAKARIERL GCGEEG 350
AAG06957      (108) AAAAKLTLLDAPVSGGVGGAR GTLSFIVGGPAEGFARARP LEN GRN
Consensus     (301) A A AG V P R I M

AAA25891     (344) 351 AQLLLDGRYKVEGYPDGNW GPTFGVRPDMAIYEE FGPVLC LAEV 400
AAG06957      (158) IFHAGDHGQVAKICNNML GILATAEALALGVNG DPAVLSEVMK
Consensus     (351) D A V LG L A K L VL

AAA25891     (394) 401 DSLEQAIRLINESP GNGTSIFTSGAARTFQHHIEVGQGGN PIPVP 450
AAG06957      (208) QSSGGN WALNLYNP PGVMPQAPSN YAGGFQVR MNKDGA ANAQA
Consensus     (401) S L PW AS A A FQ I LGI I

AAA25891     (444) 451 PFFFTGWKSFYGDHAY--K-QGRFYETKTVT WFDSDSVAGT 500
AAG06957      (258) QASPLGALRNLFSLHAQDAEHEGDFSSIQKLYRSD-----
Consensus     (451) L S G A LHA A GL F S K AK

AAA25891     (491) 501 NFSIQMR
AAG06957      (299) -----
Consensus     (501)

```

	AAA25891	AAG06957
AAA25891		14
AAG06957		

Sequence Alignment: alanine 2,3-aminomutase

			1	50
B. subtilis - SEQ. 22	(1)	MKNKWKYKPKRHWKEIELWQDVPEEWWDVWQWLTHTVRTLDDLKKVINLT		
B. subtilis - SEQ. 24	(1)	MKNKWKYKPKRHWKEIELWQDVPEEWWDVWQWLTHTVRTLDDLKKVINLT		
P. gingivalis - SEQ. 26	(1)	-----MAESRKYYIPDVTLEQWYDWHWQLNRJETLDQLKKYTLT		
Consensus	(1)	MKNKWKYKPKRHWKEIELWQDVPEEKWNVDWLQLTHTVRTLDDLKKVINLT		
			51	100
B. subtilis - SEQ. 22	(51)	E E E G V R I S K T I P L N I T P Y Y A S L M D P D N P C P V R M Q S V P L S E E M H K T K		
B. subtilis - SEQ. 24	(51)	E E E G V R I S K T I P L N I T P Y Y A S L M D P D N P C P V R M Q S V P L S E E M H K T K		
P. gingivalis - SEQ. 26	(43)	A E E E G V E S P K V R M A I T P Y Y L S L D P D N P N C P A R K O W P T Q O E V I A I		
Consensus	(51)	EDEE EGVRI STKT I PLNITPY YASLM DPDPNPRCPVRMQSVPLSEEMHKTK		
			101	150
B. subtilis - SEQ. 22	(101)	Y D M D P L E D E D S P V P G L T H R Y P D R V L F L V T N Q C S Y C R C T R R R F G Q K		
B. subtilis - SEQ. 24	(101)	Y D M D P L E D E D S P V P G L T H R Y P D R V L F L V T N Q C S Y C R C T R R R F G Q K		
P. gingivalis - SEQ. 26	(93)	E D Q V D P L S E D E D S P V P G L T H R Y P D R V L F L T D K C S Y C R C T R R R F G Q K		
Consensus	(101)	YDMEDPLHEDEDSPVPGLTHRYPDRVLFVLTNQC SVYCRHCTRRRFSGQI		
			151	200
B. subtilis - SEQ. 22	(151)	G M G V P K K Q L D A A I A Y I R E T P E I R D C L I S G G D L L I N D Q I L E Y I L K L R S I		
B. subtilis - SEQ. 24	(151)	G M G V P K K Q L D A A I A Y I R E T P E I R D C L I S G G D L L I N D Q I L E Y I L K L R S I		
P. gingivalis - SEQ. 26	(143)	D A S S P S E R D R C I D Y I A N T P T R D V L I S G G D L L S D E R L E Y I L K L R E I		
Consensus	(151)	GMGVPKKQLDAAIAYIRETP EIRDC LISGGDLLINDQILEYILKELRSI		
			201	250
B. subtilis - SEQ. 22	(201)	P H E V I R I G R T P V V F P Q R I T D L H C E I L K K Y H P V W L N T H F N T S I E M T E E S		
B. subtilis - SEQ. 24	(201)	P H E V I R I G R T P V V F P Q R I T D L H C E I L K K Y H P V W L N T H F N T S I E M T E E S		
P. gingivalis - SEQ. 26	(193)	P H E V I R I G R T P V V L P Q R I T P Q V L L K K Y H P V W L N T H F N H P N E T E E		
Consensus	(201)	PHLEVIRIGTRAPVVFPQRITDLHCEILKKYHPVWLNTHFNTSIEMTEES		
			251	300
B. subtilis - SEQ. 22	(251)	V E A C E K L V N A G V P V G N Q A V V L G I N D S V P I M K K L M H D L V K I R V R P Y Y I Y		
B. subtilis - SEQ. 24	(251)	V E A C E K L V N A G V P V G N Q A V V L G I N D S V P I M K K L M H D L V K I R V R P Y Y I Y		
P. gingivalis - SEQ. 26	(243)	V E A C E K L V N A G V P V G N Q T V L R G I N D C T H M K L L H L L V K I R V R P Y Y I Y		
Consensus	(251)	VEACEKLVNAGVPVGNOAVVLGINDSVIPMKKLMHDLVKIRVRPPYYIQ		
			301	350
B. subtilis - SEQ. 22	(301)	C D L S G I G H F R A P V S K G L E I I E L R G H T S G Y A V P T F V V H A P G G G K I A L Q		
B. subtilis - SEQ. 24	(301)	C D L S G I G H F R A P V S K G L E I I E L R G H T S G Y A V P T F V V H A P G G G K I A L Q		
P. gingivalis - SEQ. 26	(293)	C D L S G I G H F R T P V S K G L E I I E N L R G H T S G Y A V P T F V V G A P G G G K I P T		
Consensus	(301)	CDLSEGIGHFRAPVSKGLEII E LRGHTSGYAVPTFVVHAPGGGGKIALQ		
			351	400
B. subtilis - SEQ. 22	(351)	P N Y V L S Q S P D K V I L R N F E G V I T S Y P E P E N Y I P N Q A D A Y F E S V F P E T A D K K		
B. subtilis - SEQ. 24	(351)	P N Y V L S Q S P D K V I L R N F E G V I T S Y P E P E N Y I P N Q A D A Y F E S V F P E T A D K K		
P. gingivalis - SEQ. 26	(343)	P N Y V L S Q S P R H V L R N F E G V I T S Y T E P E -----N Y E E C D C E C R A G K		
Consensus	(351)	PNYVLSQSPDKVILRNFEGVITSYPEPENYIPNQADAYFESVF PETADKK		
			401	450
B. subtilis - SEQ. 22	(401)	E P I G L S A I F A D K E V S F T P E N V D R I K R R E A Y I A N P E H E T L K D R R E K R D Q L K		
B. subtilis - SEQ. 24	(401)	E P I G L S A I F A D K E V S F T P E N V D R I K R R E A Y I A N P E H E T L K D R R E K R D Q L K		
P. gingivalis - SEQ. 26	(386)	H K E G L A S G O O I E P S D A R K K R K -- D K N -----		
Consensus	(401)	EPIGLSAIFADKEVSFTPENVDRIKRREAYIANPEHETLKDRREKRDQLK		
			451	471
B. subtilis - SEQ. 22	(451)	E K K F L A O O K K O K E T E C G G D S S		
B. subtilis - SEQ. 24	(451)	E K K F L A O O K K O K E T E C G G D S S		
P. gingivalis - SEQ. 26	(417)	-----		
Consensus	(451)	EKKFLAOOKKOKETECGGDSS		

	B. subtilis – SEQ. 22	B. subtilis – SEQ. 24	P. gingivallis – SEQ. 26
B. subtilis – SEQ. 22		100	59
B. subtilis – SEQ. 24			59
P. gingivallis – SEQ. 26			